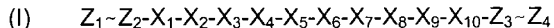


Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): An isolated compound which inhibits pilus assembly, said compound comprising a mimic of a chaperone G₁ beta-strand or a mimic of an amino terminal motif of a pilus subunit, **wherein the mimic is with at least two alternating hydrophobic amino acid residues, or** a 10 to 20 residue peptide according to formula (I):



or a pharmaceutically-acceptable salt thereof, wherein:

Z₁ is R-C(O)-NR- or RRN-;

Z₂ is an optional 1 to 5 residue peptide **or peptide analog, 1 to 5 residue peptide analog, or 1 to 5 residues consisting of both peptide and peptide analog residues;**

X₁ is any amino acid residue;

X₂ is any amino acid residue;

X₃ is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X₄ is any amino acid residue;

X₅ is a hydrophobic residue or Gly;

X₆ is a hydrophobic or a hydrophilic residue;

X₇ is Gly, an amide-substituted polar residue or a hydrophobic residue;

X₈ is **any an** amino acid residue **other than an aliphatic residue;**

X₉ is an aliphatic residue;

X₁₀ is any amino acid residue;

Z_3 is an optional 1 to 5 residue peptide ~~or peptide analog, 1 to 5 residue~~
peptide analog, or 1 to 5 residues consisting of both peptide and peptide analog
residues;

Z_4 is $-C(O)OR$ or $-C(O)NRR$;

each R is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl
or (C_6-C_{14}) aryl;

each "-" between residues X_1 through X_{10} , Z_2 and X_1 and X_{10} and Z_3
independently represents an amide linkage, a substituted amide linkage or an isostere
of an amide linkage; and

each "~" represents a bond.

Claim 2 (original): The compound of claim 1 wherein the compound is a peptide.

Claim 3 (cancelled)

Claim 4 (currently amended): The compound of claim 1 wherein the compound mimic
~~comprises a mimic of a chaperone G_4 beta-strand with at least two alternating~~
~~hydrophobic amino acid residues which~~ exhibits antibacterial activity against a
Gram-negative bacterium.

Claim 5 (currently amended): The compound of claim 4 wherein said mimic **further**
comprises ~~the amino acid sequence NVLQIAL (SEQ ID NO: 1)~~ SEQ ID NO: 1 or an
analogue thereof.

Claim 6 (cancelled)

Claim 7 (cancelled)

Claim 8 (currently amended): The compound of claim 1 wherein the compound mimic comprises a mimic of an amino terminal motif of a pilus subunit selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 9 (currently amended): The compound of claim 8 wherein said mimic of an amino-terminal motif of a pilus subunit further comprises the amino acid sequence SDVAFRGNLL (SEQ ID NO: 12) or an analogue thereof.

Claim 10 (cancelled)

Claim 11 (cancelled):

Claim 12 (cancelled)

Claim 13 (currently amended): The compound of claim ~~1~~ **12** ~~wherein said compound further comprises one or more features selected from the group consisting of~~ **wherein one or more of the following conditions are satisfied:**

each "-" between residues X_1 through X_{10} , Z_2 and X_1 and X_{10} and Z_3 is an amide linkage;

Z_1 is H_2N- ;

Z_4 is $-C(O)OH$ or a salt thereof;

optional Z_2 is not present;

optional Z_3 is not present;

X_1 is an amino acid residue other than a basic residue;

X₂ is an amino acid residue other than an aliphatic residue;

X₃ is an aliphatic residue or T;

X₄ is an amino acid residue other than an acidic residue;

X₅ is an aliphatic residue, F or G;

X₇ is G, N or A; or

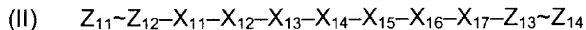
~~X₈ is other than an aliphatic residue; and~~

X₁₀ is an aliphatic or a polar residue.

Claim 14 (currently amended): The compound of claim 13 ~~which is wherein the~~
mimic comprises a sequence selected from the group consisting of SEQ ID NO: 2,
SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID
NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO:
14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19,
SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24,
SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 15 (cancelled):

Claim 16 (currently amended): An isolated compound which inhibits pilus
assembly, the compound comprising a mimic of a chaperone G₁ beta-strand or a
mimic of an amino terminal motif of a pilus subunit, wherein the mimic ~~The~~
~~antibacterial compound of claim 1 which~~ is a 7 to 17 residue peptide or peptide
analog according to formula (II):



or a pharmaceutically-acceptable salt thereof, wherein:

Z₁₁ is R'-C(O)-NR'- or R'R'N-;

Z₁₂ is an optional 1 to 5 residue peptide ~~or peptide analog, 1 to 5~~
residue peptide analog, or 1 to 5 residues consisting of both peptide and
peptide analog residues;

X₁₁ is any amino acid residue;

X₁₂ is any amino acid residue;

X₁₃ is a hydrophobic residue;

X₁₄ is any amino acid residue;

X₁₅ is a hydrophobic residue;

X₁₆ is any amino acid residue;

X₁₇ is hydrophobic residue or a hydroxyl-substituted aliphatic residue;

Z₁₃ is an optional 1 to 5 residue peptide ~~or peptide analog~~, 1 to 5 residue peptide analog, or 1 to 5 residues consisting of both peptide and peptide analog residues;

Z₁₄ is $-C(O)OR'$ or $-C(O)NR'R'$;

each R' is independently hydrogen, (C₁-C₆) alkyl, (C₂-C₆) alkenyl, (C₂-C₆) alkynyl or (C₆-C₁₄) aryl; and

each "-" between residues X₁₁ through X₁₇, Z₁₂ and X₁₁ and X₁₇ and Z₁₃ independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and each "~" independently represents a bond.

Claim 17 (original): The compound of claim 16 ~~wherein said compound further comprises one or more features selected from the group consisting of wherein one or more of the following conditions are satisfied:~~

each "-" between residues X₁₁ through X₁₇, Z₁₂ and X₁₁ and X₁₇ and Z₁₃ is an amide linkage;

Z₁₁ is H₂N-;

Z₁₄ is $-C(O)OH$ or a salt thereof;

optional Z₁₂ is not present;

optional Z₁₃ is not present;

X₁₁ is an amino acid residue other than a basic residue;

X₁₃ is an aliphatic residue or M;

X₁₄ is an amino acid residue other than an aromatic residue;

X₁₅ is an aliphatic residue, F or M; and

X₁₇ is an aliphatic residue, F, M or a hydroxyl-substituted aliphatic residue.

Claim 18 (cancelled)

Claim 19 (currently amended): The compound of any one of claims 1, 2, 5, 8, 9, 13, 14, 16, or 17 ~~claim 16~~ wherein said compound exhibits antibacterial activity against one or more a Gram-negative bacterium selected from the group consisting of comprising *E. coli*, *H. influenzae*, *S. euteriditis*, *S. typhimurium*, *B. pertussis*, *Y. pestis*, *Y. enterocolitica*, *H. pylori* and *K. pneumoniae*.

Claims 20-135 (cancelled)

Claim 136 (currently amended): An isolated compound which inhibits pilus assembly, the compound consisting of SEQ ID NO: 12. ~~The compound of claim 1 wherein the compound consists of SEQ ID NO:12.~~

Claim 137 (new): An isolated compound which inhibits pilus assembly, the compound consisting essentially of SEQ ID NO: 12, wherein the compound is a mimic of a chaperone G₁ beta-strand or a mimic of an amino terminal motif of a pilus subunit.

Claim 138 (new): An isolated compound which inhibits pilus assembly, the compound comprising a mimic of a chaperone G₁ beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic comprises SEQ ID NO:12.

Claim 139 (new): The compound of claim 138 wherein the compound competitively binds to a pilus subunit hydrophobic groove.

Claim 140 (new): A complex comprising a pilus subunit with a hydrophobic groove and a synthetic compound bound thereto; the synthetic compound competitively binding the hydrophobic groove and inhibiting pilus assembly; the synthetic compound comprising a mimic of a chaperone G1 beta-strand or a mimic of an amino terminal motif of a pilus subunit; the mimic comprising at least two independently selected hydrophobic amino acid residues; and the hydrophobic amino acid residues separated by at least one interposing independently selected amino acid; wherein the hydrophobic amino acid residues facilitate binding with the hydrophobic groove of the pilus subunit.

Claim 141 (new): The complex of claim 140 wherein the synthetic compound is any one compound of claims 1, 2, 4, 5, 8, 9, 13, 14, 16, 17, 19, or 136-139.

Claim 142 (new): The complex of claim 140 wherein the mimic comprises at least three independently selected hydrophobic amino acid residues, the hydrophobic amino acid residues separated by at least one interposing independently selected amino acid.

Claim 143 (new): The complex of claim 140 wherein the mimic comprises at least four independently selected hydrophobic amino acid residues, the hydrophobic amino acid residues separated by at least one interposing independently selected amino acid.

Claim 144 (new): The complex of claim 140 wherein the mimic comprises at least five independently selected hydrophobic amino acid residues, the hydrophobic amino acid residues separated by at least one interposing independently selected amino acid.

Claim 145 (new): The complex of claim 140 wherein at least one interposing amino acid residue is an interposing hydrophobic amino acid residue.

Claim 146 (new): The complex of claim 145 with at least two interposing hydrophobic amino acid residues.

Claim 147 (new): The complex of claim 140 wherein the mimic comprises at least five consecutive hydrophobic amino acid residues.

Claim 148 (new): The complex of claim 140 wherein the mimic comprises a core sequence derived from a chaperone G₁ beta-strand or an amino terminal motif of a pilus subunit, the core sequence comprising about 3 to about 12 residues.

Claim 149 (new): The complex of claim 148 wherein the core sequence comprises about 4 to about 9 residues.

Claim 150 (new): The complex of claim 148 wherein the core sequence comprises about 7 residues.

Claim 151 (new): The complex of claim 148 wherein the core sequence is at least about 90% identical to a sequence from a chaperone G₁ beta-strand or an amino terminal motif of a pilus subunit.

Claim 152 (new): The complex of claim 148 wherein the core sequence is at least about 80% identical to a sequence from a chaperone G₁ beta-strand or an amino terminal motif of a pilus subunit.

Claim 153 (new): The complex of claim 148 wherein the core sequence is at least about 70% identical to a sequence from a chaperone G₁ beta-strand or an amino terminal motif of a pilus subunit.

Claim 154 (new): The complex of claim 140 wherein the compound exhibits antibacterial activity against a Gram-negative bacterium.

Claim 155 (new): The complex of claim 140 wherein the mimic comprises SEQ ID NO: 1 or an analog thereof.

Claim 156 (new): The complex of claim 140 wherein the mimic comprises SEQ ID NO: 12 or an analog thereof.

Claim 157 (new): The complex of claim 140 wherein the mimic comprises a sequence at least about 80% identical to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 158 (new): The complex of any one of claims 140, 142-157 wherein the compound exhibits antibacterial activity against one or more Gram-negative bacterium selected from the group consisting of *Escherichia coli*, *Haemophilus influenzae*, *Salmonella enteritidis*, *Salmonella typhimurium*, *Bordetella pertussis*, *Yersinia pestis*, *Yersinia enterocolitica*, *Helicobacter pylori* and *Klebsiella pneumoniae*.